SUBJECT INDEX TO VOLUME 34, 1988

[A]

acetylene reduction activity 127
L-acofriose 27
activated sludge bacteria 39
Aeromonas hydrophila 355
Agromonas oligotrophica 349, 355
algal bloom 417
algal extracellular products 417
6-amino penicillanic acid 333
anaerobic bacteria 297
anaerobic digestion of municipal wastewater 425
anaerobic growth 85
anaerobic respiration 105
anaerobic treatment 297
antimony (III) 439
Arrhenius plot 209
ascomycetous yeasts 165
Asterionella glacialis 417

[B]

Bacillus circulans MH-K1 255
Bacillus subtilis 367, 451
Bacteroides fragilis 377
Bacteroides ureolyticus 85
ballistosporous yeast genus 433
basidiomycetous yeasts ..119, 165, 271, 279, 387
beneficiation magnesite ore 233
Bensingtonia ciliata, enzyme patterns of .. 289
Bradyrhizobium japonicum 243
branched-chain amino acid transport systems 183
Bullera 95

[C]

Candida 221
Candida palmioleophila sp. n. 493
Candida yeast 409
cellular fatty acid composition 67
cellulase 321
Chaetomium thermophile, polyphenol oxidase of 401
chemotaxis 417
chemotaxonomy 119, 271, 279
chemotaxonomy of actinomycetes 445
chitosan degradation 255
chitosanase from *B. circulans* 255
classification 467
coliforms antibiotic resistance metal tolerance 391
colony-morphology switching 409
colorless variant 387
cyanophage AS-1 resistant mutant 1
cytochrome spectra 221
cytochromes 85
Cystofilobasidium infirmominiatum, comb. nov. 271
Cystofilobasidium species, enzyme patterns of 201

[D]

DAPI staining 485
Deinococcus radiodurans 209
dextran 213
dextransucrase 213
dimethyl sulfoxide 105
distribution of xylose in ballistosporous yeasts 95
dot hybridization 191
double entrapment 333

[E]

electrophoretic comparison of enzymes 387
ELISA extracellular yeast antigens 15
emendation of *Bensingtonia* 433
enzyme patterns, of Q_9-equipped *Sporobolomyces* and *Bensingtonia* species 289
enzyme patterns, of *Mrakia* species 201
Erythrobacter longus 67
Erythrobasidium hasegawae, gen. nov. et sp. nov. 279
Q_9-equipped *Sporobolomyces* species, enzyme patterns of 289
Escherichia coli 475
extracellular proteinases 467

[F]

fatty acid composition of rumen bacteria .. 303
Fellomyces nectairei 503
filobasidiaceous yeast genera 279
fumarate 105
fumarate reduction 85

[G]

genus *Gordona* 341
genus *Monascus* 467
genus *Rhodococcus* 341
Geotrichum candidum extracellular polysaccharide ELISA 15
gliding bacteria 57
glutamate dehydrogenase 377
Glycine max 243

[H]

Hansenula wickerhamii extracellular polysaccharide ELISA 15
hemolysin 439
herbicides 243
hydroxy fatty acid 57, 67
HPLC 445
HPLC method for analysis of xylose in whole cell hydrolysates 95
hyperthermia 209

[I]

identification 191
immunology extracellular yeast antigens .. 15
international code of botanical nomenclature Article 59 271
iron-oxidizing bacteria 27
isocitrate dehydrogenase isozyme 457

[K]

Kurtzmanomyces gen. nov. 503
Kurtzmanomyces nectairei comb. nov. 503

[L]

laccase, of *Chaetomium thermophile* 401
Legionella 191
Leptospirillum ferrooxidans 27
Leucosporodium species, enzyme patterns of 201
Leuconostoc mesenteroides 213
lipopolysaccharide 27
lyophilization 7

[M]

madurose 445
Malbranchea pulchella var. *sulfurea* 333
membrane proteins, of *B. subtilis* 367
menaquinone 39
methane-producing bacteria 297
methanogenesis 425
microbial silica removal 233
mitochondrial nucleoids 485
mpo mutation, of *B. subtilis* 367
Mrakia species, enzyme patterns of 201
municipal wastewater, anaerobic digestion of 425
mutant defective in isocitrate dehydrogenase 457
myxobacteria 57
Myxomycetes 321

[N]

N_2 fixation 243
new combinations of yeasts 433, 499
nitrate 105
nitrate respiration 475
nitrogen fixation 127
nitrogen-fixing bacteria 127

[O]

oligotrophic bacteria 349, 355
oxalic acid 111
oxidation of fatty acids 297

[P]

palm oil-utilizing yeast 493
parameters for silica removal 233
pectinase 321
penicillin acylase 333
pH-activity profiles 467
phosphatidylethanolamine 57
photobiotin 191
photoreductio of DCPIP 1
photosystem II, copper inhibition 1
phragmometabasidium 119
phylogeny of actinomycetes 341
plasmids 111
polyphenol oxidase, of *Chaetomium thermophile* 401
presence of xylose in *Itersonilia perplexans* .. 95
preservation of *Streptomyces* 7
properties of chitosanase 255
Pseudomonas sp. 417
psychrophilic bacteria 457
pulse-field gel electrophoresis 409
purification 377
purification of chitosanase 255
pyrophosphatidic acid in yeasts 165

[Q]

quinone profiles 39

[R]

radioresistant bacterium 209
repression of transport activity 183
reversible inactivation 377
reverse transcriptase 341
ribosomal RNA sequence analyses 341
Rhizoctonia solani 111
rhizosphere of rice 127
Rhodospirillaceae genera 67
Rhodosporidium infirmominiatum, enzyme patterns of 201
Rhodosporidium kratochvilovae sp. nov. 119
Rhodosporidium toruloides 119
Rhodotorula hasegawa 279

[S]

Saccharomyces cerevisiae 485
Saccharomyces cerevisiae extracellular polysaccharide ELISA 15
Salmonella typhimurium LT2 183
sclerotium 111
self-sporulating yeasts 119
sephadex 213
silica solubilising bacillus 233
silica removal from magnesite 233
spo0A expression 451
spo0F function 451
Sporobolomyces 95
Sporobolomyces intermedius, enzyme patterns of 289
Sporobolomyces phylladus, enzyme patterns of 289
Sporobolomyces salicinus comb. n. 499
Sporobolomyces tsugae comb. n. 499
sporulation inhibition 451
Stephanoascus ciferrii extracellular polysaccharide ELISA 15
Sterigmatomyces nectairei 503
Sterigmatomyces wingfieldii 507
Streptococcus bovis 213
Streptococcus pyogenes 439
streptolysin S 439
sugar composition of rumen bacteria 303
sulfhydryl compound 439
sulfate reduction 425
sulfate-reducing bacteria 297
superoxide dismutase 105, 475

[T]

taxonomy 221
teliospore-forming yeasts 271, 387
thermotolerance induction 209
Thiobacillus ferrooxidans 27
transport mutants of *Salmonella typhimurium* 183
trimethylamine N-oxide 105
Tsuchiyaea gen. nov. 507
Tsuchiyaea wingfieldii comb. nov. 507

[U]

ubiquinone 39

[V]

Vibrio 457

[W]

whole cell immobilization 333
whole-cell sugar 445

[X]

xylanase 321
xylose content, in cells of *Sterigmatomyces* .. 507
xylose content, in cells of *Sterigmatomyces* and *Fellomyces* 503

[Y]

yeast 221, 485